

Appl. No. : **10/009,792**
Filed : **December 13, 2001**

REMARKS

This is in response to the Notice to Comply with Requirements for Patent Applications containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures mailed August 12, 2004. The notice indicated that the sequence "AGPHHHHHH" in amended Claim 3 was not identified by a sequence identification number.

Applicants have amended Claim 3 to remove this term and to clarify the claimed subject matter. In addition, new dependent claims 11-13 have been added to further clarify the nucleotide sequences recited in Claim 3. No new matter has been added by these amendments. Accordingly, as this language was removed from Claim 3, Applicants do not need to submit a substitute Sequence Listing.

Lack of Unity Rejection

Applicants would like to take the opportunity to again explain the relationship between the claimed sequences in order to clarify the issue for the Examiner. The Examiner previously restricted the claims into Group I, Claims 1, 2, and 7-10 and Group II, Claims 3-6.

Claim 3 recites a nucleotide sequence that encodes the oligopeptide of SEQ ID NO: 1. As previously argued, SEQ ID NO: 1 comprises 13 amino acids and includes two domains. The first domain is a HIS tag region comprising the sequence AGPHHHHHH. The second domain is a protease target sequence comprising the sequence IEGR.

Claim 1 recites a nucleotide sequence coding for an oligopeptide consisting of 13 amino acids, including six consecutive histidine residues. Thus, the amino acid sequence recited in SEQ ID NO: 1 is simply an example of an oligopeptide claimed in Claim 1. For this reason, in order for the Examiner to properly search the invention recited in Claim 1, she would necessarily have to search nucleotide sequences that encode SEQ ID NO: 1.

Claim 2, which depends from Claim 1, simply defines the oligopeptide to include the protease target sequence "IEGR" (SEQ ID NO: 28). As this IEGR sequence is also found within the 13 amino acids of SEQ ID NO: 1, any search for oligopeptides having SEQ ID NO: 1 would also entail a search of the protease target sequence of SEQ ID NO: 28.

For all of these reasons, the claimed vectors share significant structural features. Moreover, any search of the sequences recited in Claim 1 would necessarily include a search of the sequences recited in Claim 3. Thus, it would not place a burden on the Examiner to examine

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Group I and Group II together. Accordingly, Applicants traverse the pending restriction requirement and respectfully request examination of all pending claims.

Support for New Claims

Applicants have added new Claims 11-13 to more specifically define the sequences recited in Claim 3. For example, new Claim 11 recites that the vector comprises the nucleotide sequence of SEQ ID NO: 26. This sequence was in the Sequence Listing as originally filed, and thus is not new matter.

New Claim 12 recites that modified gene comprises nucleotides 88 to 610 of SEQ ID NO: 18 and encodes the hG-CSF amino acid sequence of SEQ ID NO: 19. Support for this amendment can be found in Figure 3, which shows the mature hG-CSF protein as being encoded from nucleotides 88-610 of SEQ ID NO: 18. The mature hG-CSF protein shown in Figure 3 is recited in SEQ ID NO: 19. As Figure 3 was in the application as filed, this new claim does not add any new matter.

New Claim 13 recites that the nucleotide sequence coding for the endoxylanase signal sequence comprises nucleotides 1-84 of SEQ ID NO: 26. As stated at page 15, lines 32-36, Figure 12 illustrates the coding sequence for the endoxylanase signal as italicized. The DNA sequence in Figure 12 is found in SEQ ID NO: 26. Nucleotides 1-84 of SEQ ID NO: 26 correspond to the italicized nucleotides from Figure 12. As such, reference to these nucleotides are not new matter, as this sequence was readily apparent from Figure 12 as filed.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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